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APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/709,905	11/10/2000	Kalyanaraman Ramnarayan	24737-1906C

STEPHANIE L. SEIDMAN, ESQ.
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4350 LA JOLLA VILLAGE DRIVE
SAN DIEGO, CA 92122-1246



CONFIRMATION NO. 3606
FORMALITIES LETTER



OC000000006275717

Date Mailed: 07/10/2001

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
DISCLOSURES**

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

- For Rules Interpretation, call (703) 308-4216
- To Purchase PatentIn Software, call (703) 306-2600
- For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov

A copy of this notice MUST be returned with the reply.

Allyn

Customer Service Center

Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE

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BIOTECHNOLOGY
SYSTEMS
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RAW SEQUENCE LISTING ERROR REPORT

SEP 17 2001

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

Application Serial Number: 09/709,905

Source: OIPE

Date Processed by STIC: 3/13/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER (703-308-4212)

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX (703-308-4210)

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE SEE BELOW

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual

Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS based version of Checker and is Y2K compliant. Checker allows public users to check sequence listings for Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



OIPC

RAW SEQUENCE LISTING DATE: 03/13/2001
 PATENT APPLICATION: US/09/709,905 TIME: 15:05:04

Input Set : A:\1906cseq.002
 Output Set: N:\CRF3\03132001\I709905.raw

4 <110> APPLICANT: Kalyanaraman Ramnarayan
 5 Edward T. Maggio
 6 P. Patrick Hess
 9 <120> TITLE OF INVENTION: Use of Computationally Derived Protein
 10 Structures of Genetic Polymorphisms in Pharmacogenomics for
 11 Drug Design and Clinical Applications
 15 <130> FILE REFERENCE: 24737-1906C
 OK > 17 <140> CURRENT APPLICATION NUMBER: US/09/709,905
 18 <141> CURRENT FILING DATE: 2000-11-10
 20 <150> PRIOR APPLICATION NUMBER: 09/438,566
 21 <151> PRIOR FILING DATE: 1999-11-10
 23 <150> PRIOR APPLICATION NUMBER: 24737-1906B
 24 <151> PRIOR FILING DATE: 2000-11-01
 26 <160> NUMBER OF SEQ ID NOS: 118
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 6
 32 <212> TYPE: PRT
 33 <213> ORGANISM: Artificial Sequence
 35 <220> FEATURE:
 36 <223> OTHER INFORMATION: Modified Hepatitis C Virus NS3 Protease Inhibitor
 37 Peptide
 40 <221> NAME/KEY: ACETYLATION
 41 <222> LOCATION: 1
 43 <221> NAME/KEY: MOD_RES
 44 <222> LOCATION: 2
 45 <223> OTHER INFORMATION: D-glutamic acid
 47 <221> NAME/KEY: MOD_RES
 48 <222> LOCATION: 5
 49 <223> OTHER INFORMATION: beta-cyclohexylalanine
 51 <300> PUBLICATION INFORMATION:
 52 <301> AUTHORS: Ingallinella, P., Altamura, S., Bianchi, E., Talia
 53 <302> TITLE: Potent Peptide Inhibitors Of Human Hepatitis C Vir
 54 <303> JOURNAL: Biochemistry
 55 <304> VOLUME: 37
 56 <305> ISSUE: 25
 57 <306> PAGES: 8906-8914
 58 <307> DATE: 1998-06-23
 OK > 60 <400> SEQUENCE: 1
 61 Asp Xaa Leu Ile Xaa Cys
 62 1 5
 64 <210> SEQ ID NO: 2
 65 <211> LENGTH: 6
 66 <212> TYPE: PRT
 67 <213> ORGANISM: Artificial Sequence
 69 <220> FEATURE:
 70 <223> OTHER INFORMATION: Modified Hepatitis C Virus NS3 Protease Inhibitor

pp. 2 4-5

Does Not Comply
 Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/709,905

DATE: 03/13/2001
TIME: 15:05:04

Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw

71 Peptide
 75 <221> NAME/KEY: ACETYLATION
 76 <222> LOCATION: 1
 78 <221> NAME/KEY: MOD_RES
 79 <222> LOCATION: 5
 80 <223> OTHER INFORMATION: beta-cyclohexylalanine
 82 <300> PUBLICATION INFORMATION:
 83 <301> AUTHORS: Ingallinella, P., Altamura, S., Bianchi, E., Talia
 84 <302> TITLE: Potent Peptide Inhibitors Of Human Hepatitis C Vir
 85 <303> JOURNAL: Biochemistry
 86 <304> VOLUME: 37
 87 <305> ISSUE: 25
 88 <306> PAGES: 8906-8914
 89 <307> DATE: 1998-06-23
 91 <400> SEQUENCE: 2
 W-> 92 Asp Glu Leu Ile Xaa Cys
 93 1 5
 95 <210> SEQ ID NO: 3
 96 <211> LENGTH: 1045
 97 <212> TYPE: DNA
 98 <213> ORGANISM: Human Immunodeficiency Virus (HIV)
 100 <220> FEATURE:
 101 <221> NAME/KEY: CDS (1) ← coding begins at first base (global error)
 W-> 102 <222> LOCATION: (10)...(297)
 103 <223> OTHER INFORMATION: Protease
 105 <221> NAME/KEY: CDS
 W-> 106 <222> LOCATION: (298)...(1045)
 107 <223> OTHER INFORMATION: Portion of Reverse Transcriptase
 109 <400> SEQUENCE: 3
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 W-> 111 Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
 112 1 5 10 15
 114 ggc caa cta aaa gaa gct yta tta gat aca gga gca gat gat aca gta 96
 115 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
 116 20 25 30
 118 tta gaa gaa atg agt tta cca ggg aaa tgg aaa ccā aaa atg ata ggg 144
 119 Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 120 35 40 45
 122 gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata ctc ata 192
 123 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
 124 50 55 60
 126 gaa atc tgt gga cat aaa gct ata ggc aca gta gta gga cct aca 240
 127 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 128 65 70 75 80
 130 cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act 288
 131 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 132 85 90 95
 134 tta aat ttg ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 135 Leu Asn Leu Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/709,905

DATE: 03/13/2001
TIME: 15:05:04

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Output Set: N:\CRF3\03132001\I709905.raw

136	100	105	110	
138	cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa			384
139	Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu			
140	115	120	125	
142	aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga			432
143	Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Clu Lys Glu Gly			
144	130	135	140	
146	aaa att tca aaa att ggg cct gag aat cca tac aat act cca ata ttt			480
147	Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe			
148	145	150	155	160
150	gcc ata aag aaa aaa gac ayt act aaa tgg aga aaa tta gta gat ttc			528
151	Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe			
152	165	170	175	
154	aga gaa ctt aat aag aga aca caa gac ttc tgg gaa gtt caa tta gga			576
155	Arg Glu Leu Asn Lys Arg Thr Glu Asp Phe Trp Glu Val Gln Leu Gly			
156	180	185	190	
158	ata cca cac ccc gca ggg tta aaa cag aaa aaa tca gta aca ata ctg			624
159	Ile Pro His Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Ile Leu			
160	195	200	205	
162	qat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa ggc ttc agg			672
163	Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg			
164	210	215	220	
166	aag tat act gca ttt acc ata cct agt aga aat aat gag aca cca qgg			720
167	Lys Tyr Thr Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly			
168	225	230	235	240
170	att aga tat cag tac aac gtg ctc cca cag gga tgg aaa gga tca cca			768
171	Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
172	245	250	255	
174	gca ata ttt caa agt agc atg aca aga aty tta gag cct ttt aga aaa			816
175	Ala Ile Phe Gln Ser Ser Met Thr Arg Xaa Leu Glu Pro Phe Arg Lys			
176	260	265	270	
178	caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta			864
179	Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val			
180	275	280	285	
182	gga tct gac tta gaa ata gga cag cat aga gca aaa ata gag gaa ctg			912
183	Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu			
184	290	295	300	
186	aga gga cat cta tta aag tgg gga ttt acc aca cca gac aaa aaa cat			960
187	Arg Gly His Leu Leu Lys Trp Gly Phe Thr Pro Asp Lys Lys His			
188	305	310	315	320
190	cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat			1008
191	Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
192	325	330	335	
194	aaa tgg aca gta cag cct ata aag ttg cca gaa aaa g			1045
195	Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys			
196	340	345		
199	<210> SEQ ID NO: 4			
200	<211> LENGTH: 1046			
201	<212> TYPE: DNA			

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/709,905

DATE: 03/13/2001
TIME: 15:05:04

Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw

202 <213> ORGANISM: Human Immunodeficiency Virus (HIV)
 204 <220> FEATURE:
 205 <221> NAME/KEY: CDS (1) *←*
 W--> 206 <222> LOCATION: (0) ... (297)
 207 <223> OTHER INFORMATION: HIV Protease
 209 <221> NAME/KEY: CDS
 W/ 210 <222> LOCATION: (298) ... (1046)
 211 <223> OTHER INFORMATION: Portion of HIV Reverse Transcriptase
 213 <400> SEQUENCE: 4
 214 cct cag atc act ctt tgg caa cga ccc ctt gtc aca atu aag ata gga 48
 215 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
 216 1 5 10 15
 218 ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 219 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 220 20 25 30
 222 gtt gaa qaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144
 223 Val Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 224 35 40 45
 226 gga att gga ggt ttt atc aaa gta aga cag tat gag caa ata gcc gta 192
 227 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile Ala Val
 228 50 55 60
 230 gaa aty tgt gga cat aga gci atg ggt aca gta tta gta ggg cct aca 240
 W/ 231 Glu Xaa Cys Gly His Arg Ala Met Gly Thr Val Leu Val Gly Pro Thr
 232 65 70 75 80
 234 ccc gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 235 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 236 85 90 95
 238 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 239 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 240 100 105 110
 242 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 243 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 244 115 120 125
 246 aaa ata aaa gca tta gta gaa atc tgt aca gaa ttg gaa aag gaa ggg 432
 247 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 248 130 135 140
 250 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 251 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 252 145 150 155 160
 254 gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttg 528
 255 Ala Ile Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 256 165 170 175
 258 aga gaa ctt aat aag aga act caa gac ttc tgg gag gtt caa tta gga.
 259 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 260 180 185 190
 262 ata cca cat cca gca ggg tta aaa aag aat aaa tca ata aca gta ctg 624
 263 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Ile Thr Val Leu
 264 195 200 205
 266 gat gtg ggt gat gca tat ttt tca gtt ccc tta tg^r gaa gac ttc agg 672

RAW SEQUENCE LISTING
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Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw

267 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Cys Glu Asp Phe Arg		
268 210 215 220		
270 aag tat act gca ttt acc ata cct aqt gta aac aat gag act cca ggg	720	
271 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly		
272 225 230 235 240		
274 att aga tat cag tac tat gty ctt cca cag gga tgg aaa gga ttc acc	768	
275 ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Phe Thr		
276 245 250 255		
278 agc ata ttc caa tgc atg aca aaa atc tta gag cct ttt aga aaa	816	
279 Ser Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys		
280 260 265 270		
282 caa aat cca gag ata gtt atc tat caa tac atg gat gat ttg tat gta	864	
283 Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val		
284 275 280 285		
286 gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg	912	
287 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu		
288 290 295 300		
290 aga caa tat ctg tgg aag tgg gga ttt tgc aca cca gaa caa aar cat	960	
291 Arg Gln Tyr Leu Trp Lys Trp Gly Phe Cys Thr Pro Glu Gln Lys His		
292 305 310 315 320		
294 cag aaa gaa cct cct ttc ctt tgg atg ggt tat gaa ctc cat ccc gat	1008	
295 Gln Lys Gln Pro Pro Phe Ile Trp Met Gly Tyr Glu Leu His Pro Asp		
296 325 330 335		
298 aaa tgg aca gta caa cct ata gtg ctg cca gac aaa ga	1046	
299 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys		
300 340 345		
303 <210> SEQ ID NO: 5		
304 <211> LENGTH: 1104		
305 <212> TYPE: DNA		
306 <213> ORGANISM: Human Immunodeficiency Virus (HIV)		
308 <220> FEATURE:		
309 <221> NAME/KEY: CDS (1)		
W--> 310 <222> LOCATION: (0)...(297)		
311 <223> OTHER INFORMATION: HIV Protease		
313 <221> NAME/KEY: CDS		
OK 314 <222> LOCATION: (298)...(1104)		
315 <223> OTHER INFORMATION: Portion of HIV Reverse Transcriptase		
317 <400> SEQUENCE: 5		
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319 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Xaa Gly		
320 1 5 10 15		
322 ggg caa cta agg gaa gct cta tta gat aca gga gca gat gat aca ata	96	
323 Gly Gln Leu Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile		
324 20 25 30		
326 ata gaa gac ata act ttg cca gga aga tgg aca cca aaa atg ata ggg	144	
327 Ile Glu Asp Ile Thr Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly		
328 35 40 45		
330 gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata	192	
331 Gly Ile Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile		

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/709,905

DATE: 03/13/2001
TIME: 15:05:05

Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application Number
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:102 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:3, CDS LOCATION: (0)...(297)
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:206 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:4, CDS LOCATION: (0)...(297)
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:310 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:5, CDS LOCATION: (0)...(297)
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:418 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:6, CDS LOCATION: (0)...(297)
L:530 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:7, CDS LOCATION: (0)...(297)
L:546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:642 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:8, CDS LOCATION: (0)...(297)
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:754 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:9, CDS LOCATION: (0)...(297)
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:866 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:10, CDS LOCATION: (0)...(297)
L:879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:935 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:943 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:978 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:11, CDS LOCATION: (0)...(297)
L:987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:991 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1090 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:12, CDS LOCATION: (0)...(297)
L:1171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1202 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:13, CDS LOCATION: (0)...(297)
L:1211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1314 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:14, CDS LOCATION: (0)...(297)
L:1387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1426 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:15, CDS LOCATION: (0)...(297)

VERIFICATION SUMMARY
 PATENT APPLICATION: US/09/709,905

DATE: 03/13/2001
 TIME: 15:05:05

Input Set : A:\1906cseq.002
 Output Set: N:\CRF3\03132001\I709905.raw

L:1443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:1447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:1499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:1515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:1523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:1538 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:16, CDS LOCATION: (0)...(297)
 L:1579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
 L:1619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
 L:1650 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:17, CDS LOCATION: (0)...(297)
 L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1762 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:18, CDS LOCATION: (0)...(297)
 L:1783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 L:1819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 L:1874 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:19, CDS LOCATION: (0)...(297)
 L:1986 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:20, CDS LOCATION: (0)...(297)
 L:2098 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:21, CDS LOCATION: (0)...(297)
 L:2210 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:22, CDS LOCATION: (0)...(297)
 L:2322 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:23, CDS LOCATION: (0)...(297)
 L:2434 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:24, CDS LOCATION: (0)...(297)
 L:2546 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:25, CDS LOCATION: (0)...(297)
 L:2658 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:26, CDS LOCATION: (0)...(297)
 L:2770 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:27, CDS LOCATION: (0)...(297)
 L:2774 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:28, CDS LOCATION: (0)...(297)
 L:2882 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:29, CDS LOCATION: (0)...(297)
 L:2994 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:30, CDS LOCATION: (0)...(297)
 L:3106 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:31, CDS LOCATION: (0)...(297)
 L:3218 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:32, CDS LOCATION: (0)...(297)
 L:3330 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:33, CDS LOCATION: (0)...(297)
 L:3442 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:34, CDS LOCATION: (0)...(297)
 L:3554 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:35, CDS LOCATION: (0)...(297)
 L:3666 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:36, CDS LOCATION: (0)...(297)
 L:3778 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:37, CDS LOCATION: (0)...(297)
 L:3890 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, CDS LOCATION: (0)...(297)
 L:4002 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:39, CDS LOCATION: (0)...(297)
 L:4114 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:40, CDS LOCATION: (0)...(297)
 L:4226 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:41, CDS LOCATION: (0)...(297)
 L:4338 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:42, CDS LOCATION: (0)...(297)
 L:4446 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:43, CDS LOCATION: (0)...(297)
 L:4550 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:44, CDS LOCATION: (0)...(297)
 L:4658 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:45, CDS LOCATION: (0)...(297)
 L:4770 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:46, CDS LOCATION: (0)...(297)
 L:4882 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:47, CDS LOCATION: (0)...(297)
 L:4994 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:47, CDS LOCATION: (0)...(297)

VERIFICATION SUMMARY DATE: 03/13/2001
PATENT APPLICATION: US/09/709,905 TIME: 15:05:05

Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw

L:5106 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:48, CDS LOCATION: (0)...(297)
L:5218 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:49, CDS LOCATION: (0)...(297)
L:5330 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:50, CDS LOCATION: (0)...(297)
L:5442 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:51, CDS LOCATION: (0)...(297)